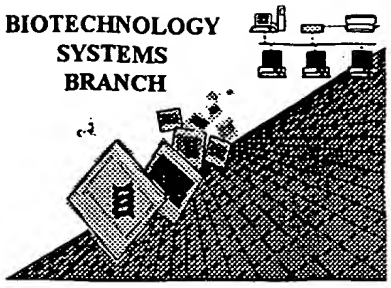
M. Walicka

BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/554,414A

Source: OIPE

Date Processed by STIC: 8/8/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/554,414A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.

11 ✓ ____Use of <220> — Sequence(s) 1-10 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

N. Walker

OIPE

RAW SEQUENCE LISTING DATE: 08/08/2001
PATENT APPLICATION: US/09/554,414A TIME: 14:15:37

Input Set : A:\Sequence listing.txt
Output Set: N:\CRF3\08082001\I554414A.raw

Does Not Comply
Corrected Diskette Needed

pp 1-5

```
     4 <110> APPLICANT: McGILL UNIVERSITY
     5       SZYF, Moshe
     6       BHATTACHARYA, Sanjoy K.
     7       RAMCHANDANI, Shyam
    10 <120> TITLE OF INVENTION: DNA DEMETHYLASE, THERAPEUTIC AND
    11       DIAGNOSTIC USES THEREOF
W--> 13 <130> FILE REFERENCE:
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/554,414A
C--> 15 <141> CURRENT FILING DATE: 2000-09-06
    15 <150> PRIOR APPLICATION NUMBER: CA 2,220,805
    16 <151> PRIOR FILING DATE: 1997-11-12
    18 <150> PRIOR APPLICATION NUMBER: CA 2,230,991
    19 <151> PRIOR FILING DATE: 1998-05-11
    21 <160> NUMBER OF SEQ ID NOS: 10
    23 <170> SOFTWARE: FastSEQ for Windows Version 3.0
    25 <210> SEQ ID NO: 1
    26 <211> LENGTH: 1804
    27 <212> TYPE: DNA
    28 <213> ORGANISM: Unknown
W--> 30 <220> FEATURE:
W--> 30 <223> OTHER INFORMATION:
    30 <400> SEQUENCE: 1
    31  ccgctctgcg ggcggggcgg gtctccggga ttccaagggc tcggttacgg aagaagcgca      60
    32  gagccggctg gggagggggc tggatgcgcg cgcacccggg gggaggccgc tgctgcccgg     120
    33  agcaggagga gggggagagc gcggcgggcg gcagcggcgc tggcggcgac tccgccatag     180
    34  agcaggggag ccagggcagc gcgctcgctc cgtccccggt gagcggcgtg cgcagggaag     240
    35  gcgctcgggg cggcggccgt ggccgggggc ggtggaagca ggcggcccgg ggcggcggcg     300
    36  tctgtggccg tggccgtggc cgtggccggg gtcggggccg tggccggggc cggggccggg     360
    37  gccgcggccg tccccagagt ggcggcagcg gccttggcgg cgacggcggc ggcggcgcgg     420
    38  gcggctgcgg cgtcggcagc ggtggcggcg tcgccccccg gcgggatcct gtccctttcc     480
    39  cgtcggggag ctcggggccg gggcccaggg gaccccgggc cacggagagc gggaagagga     540
    40  tggactgccc ggccctcccc cccggatgga agaaggagga agtgatccga aaatcagggc     600
    41  tcagtgctgg caagagcgat gtctactact tcagtccaag tggtaagaag ttcagaagta     660
    42  aacctcagct ggcaagatac ctgggaaatg ctgttgacct tagcagtttt gacttcagga     720
    43  ccggcaagat gatgcctagt aaattacaga agaacaagca gagactccgg aatgaccccc     780
    44  tcaatcagaa caagggtaaa ccagacctga acacaacatt gccaattaga caaactgcat     840
    45  caattttcaa gcaaccagta accaaattca cgaaccaccc gagcaataag gtgaagtcag     900
    46  acccccagcg gatgaatgaa caaccacgtc agcttttctg ggagaagagg ctacaaggac     960
    47  ttagcgcatc agatgtaaca gaacaaatta taaaaaccat ggagctacct aaaggtcttc    1020
    48  aaggagtcgg tccaggtagc aatgacgaga cccttctgtc tgctgtggcc agtgctttac    1080
    49  acacaagctc tgcgcccatc acaggacaag tctctgctgc cgtggaaaag aaccctgctg    1140
    50  tttggcttaa cacatctcaa cccctctgca aagctttcat tgttacagat gaagacatta    1200
    51  ggaaacagga agagcgagtc caacaagtac gcaagaaact ggaggaggca ctgatggccg    1260
    52  acatcctgtc ccgggctgcg gacacggagg aagtagacat tgacatggac agtggagatg    1320
    53  aggcgtaaga atatgatcag gtaactttcg actgaccttc cccaagagca aattgctaga    1380
    54  aacagaatta aaacatttcc actgggtttc gcctgtaaga aaaagtgtac ctgagcacat    1440
    55  agctttttaa tagcactaac caatgccttt ttagatgtat ttttgatgta tatatctatt    1500
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see item 11 on Error Summary Sheet

RAW SEQUENCE LISTING DATE: 08/08/2001
PATENT APPLICATION: US/09/554,414A TIME: 14:15:37

Input Set : A:\Sequence listing.txt
Output Set: N:\CRF3\08082001\I554414A.raw

attccaaatg atgtttattt tgaatcctag gacttaaaat gagtctttta taatagcaag 1560
cagggccctt ccggtgcagt gcagctttga ggccaggtgc agtctactgg aaaggtagca 1620
cttacgtgaa atatttgttt cccccacagt tttaatataa acagatcagg agtaccaaat 1680
aagtttccca attaaagatt attatacttc actgtatata aacagatttt tatactttat 1740
tgaaagaaga tacctgtaca ttcttccatc atcactgtaa agacaaataa atgactatat 1800
tcac 1804

<210> SEQ ID NO: 2
<211> LENGTH: 411
<212> TYPE: PRT
<213> ORGANISM: Unknown
W--> <220> FEATURE:
W--> <223> OTHER INFORMATION:
<400> SEQUENCE: 2

Same error

Met Arg Ala His Pro Gly Gly Gly Arg Cys Cys Pro Glu Gln Glu Glu
1 5 10 15
Gly Glu Ser Ala Ala Gly Gly Ser Gly Ala Gly Gly Asp Ser Ala Ile
20 25 30
Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly
35 40 45
Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Arg Trp
50 55 60
Lys Gln Ala Gly Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg
65 70 75 80
Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg
85 90 95
Pro Pro Ser Gly Gly Ser Gly Leu Gly Gly Asp Gly Gly Gly Cys Gly
100 105 110
Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Arg Arg Glu Pro Val Pro
115 120 125
Phe Pro Ser Gly Ser Ala Gly Pro Gly Pro Arg Gly Pro Arg Ala Thr
130 135 140
Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys
145 150 155 160
Lys Glu Glu Val Ile Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp
165 170 175
Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
180 185 190
Leu Ala Arg Tyr Leu Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe
195 200 205
Arg Thr Gly Lys Met Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg
210 215 220
Leu Arg Asn Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn
225 230 235 240
Thr Thr Leu Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
245 250 255
Thr Lys Val Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
260 265 270
Arg Met Asn Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln
275 280 285

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/554,414A

DATE: 08/08/2001
TIME: 14:15:37

Input Set : A:\Sequence listing.txt
Output Set: N:\CRF3\08082001\I554414A.raw

```
105  Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu
106      290                 295                 300
107  Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr
108  305                 310                 315                 320
109  Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile
110                  325                 330                 335
111  Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu
112              340                 345                 350
113  Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp
114          355                 360                 365
115  Ile Arg Lys Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu
116      370                 375                 380
117  Glu Ala Leu Met Ala Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu
118  385                 390                 395                 400
119  Met Asp Ile Glu Met Asp Ser Gly Asp Glu Ala
120                  405                 410

122 <210> SEQ ID NO: 3
123 <211> LENGTH: 1589
124 <212> TYPE: DNA
125 <213> ORGANISM: Unknown
W--> 127 <220> FEATURE:
W--> 127 <223> OTHER INFORMATION:
127 <400> SEQUENCE: 3
128  cacgcgcggg cgggtgggcg gagcggcccc cctagcgggg gctgtgaagc gcggggaggg     60
129  ggccgagcgg gtggcgaagc cggcgcgcgc ccggctgggg gcggagggcg gaggcccgtg    120
130  ggacagaaca gctgcggcga gtggcggcgg cggagggagc cgaatcggcg acgagcccgg    180
131  gggtcgcaac ttgcagaagc ggcggcggcg gcggcatcgg ccacggcggg cggaaaagcc    240
132  ggggcgcaat ggagcggaag aggtgggagt gcccggcgct cccgcagggc tgggaaaggg    300
133  aagaagtgcc caggaggtcg gggctgtcgg ccggccacag ggatgtcttt tactatagcc    360
134  ccagcgggaa gaagttccgc agcaagccac aactggcacg ttacctgggc ggatccatgg    420
135  acctcagcac cttcgacttc cgcaccggaa agatgttgat gaacaagatg aataagagtc    480
136  gccagcgtgt gcgctatgat tcttccaacc aggtcaaggg caagcctgac ctgaacaccg    540
137  cgctgcctgt acggcagact gcatccatct tcaagcaacc ggtgaccaag atcaccaacc    600
138  accccagcaa caaggtcaag agcgacccgc agaaggcagt ggaccagccg aggcagcttt    660
139  tctgggagaa gaagctaagt ggattgagtg cctttgacat tgcagaagaa ctggtcagga    720
140  ccatggactt gcccaagggc ctgcagggag tgggccctgg ctgtacagat gagacgctgc    780
141  tgtcagccat tgcgagtgct ctacacacca gcaccctgcc cattacaggc cagctctctg    840
142  cagccgtgga gaagaaccct ggtgtgtggc tgaacactgc acagccactg tgcaaagcct    900
143  tcatggtgac agatgacgac atcaggaagc aggaggagct ggtacagcag gtacggaagc    960
144  gcctggagga ggcactgatg gccgacatgc tagctcatgt ggaggagctt gcccgagacg   1020
145  gggaggcacc actggacaag gcctgtgcag aggaggaaga ggaggaggaa gaggaggagg   1080
146  aagagccgga gccagagcga gtgtagcaca ggtgccctgc ccaagtctgg gctgcagact   1140
147  gccttcagcc ttgcctggac caggtagggg ccagacctgt aggaggcagc cgtccacctc   1200
148  ctttccaaag cctcctgctt ccaggtctca gtgcagggag cccctgtgga ccttgaactc   1260
149  acttgtccct gcgctgcctg gcaggaagcc ccacactgaa agcagatgag cagtgaccca   1320
150  actgagaggc cacctggaca cagtcacctc cctgcctcct tatcatagga caaggccttg   1380
151  cttggcaccg aggagctggg agccgtgttg ggtgctggag gaagtttctg gaaacacacc   1440
152  tggctatgcc caccttatgt ccctaaggct attacaggcc agggtttgga ctgctccggc   1500
153  ccacagggct gcccagcctc cccacactga gggtcagcag cccaccagga agtcactttc   1560
```

RAW SEQUENCE LISTING DATE: 08/08/2001
PATENT APPLICATION: US/09/554,414A TIME: 14:15:37

Input Set : A:\Sequence listing.txt
Output Set: N:\CRF3\08082001\I554414A.raw

154 cttcaataaa ctgatggtag gaacttgtg 1589
156 <210> SEQ ID NO: 4
157 <211> LENGTH: 291
158 <212> TYPE: PRT
159 <213> ORGANISM: Unknown
W--> 161 <220> FEATURE:
W--> 161 <223> OTHER INFORMATION:
161 <400> SEQUENCE: 4

```
Met Glu Arg Lys Arg Trp Glu Cys Pro Ala Leu Pro Gln Gly Trp Glu
 1               5                  10                  15
Arg Glu Glu Val Pro Arg Arg Ser Gly Leu Ser Ala Gly His Arg Asp
            20                  25                  30
Val Phe Tyr Tyr Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
        35                  40                  45
Leu Ala Arg Tyr Leu Gly Gly Ser Met Asp Leu Ser Thr Phe Asp Phe
    50                  55                  60
Arg Thr Gly Lys Met Leu Met Ser Lys Met Asn Lys Ser Arg Gln Arg
65                  70                  75                  80
Val Arg Tyr Asp Ser Ser Asn Gln Val Lys Gly Lys Pro Asp Leu Asn
                85                  90                  95
Thr Ala Leu Pro Val Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
            100                 105                 110
Thr Lys Ile Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
        115                 120                 125
Lys Ala Val Asp Gln Pro Arg Gln Leu Phe Trp Glu Lys Lys Leu Ser
    130                 135                 140
Gly Leu Asn Ala Phe Asp Ile Ala Glu Glu Leu Val Lys Thr Met Asp
145                 150                 155                 160
Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Cys Thr Asp Glu Thr
                165                 170                 175
Leu Leu Ser Ala Ile Ala Ser Ala Leu His Thr Ser Thr Met Pro Ile
            180                 185                 190
Thr Gly Gln Leu Ser Ala Ala Val Glu Lys Asn Pro Gly Val Trp Leu
        195                 200                 205
Asn Thr Thr Gln Pro Leu Cys Lys Ala Phe Met Val Thr Asp Glu Asp
    210                 215                 220
Ile Arg Lys Gln Glu Glu Leu Val Gln Gln Val Arg Lys Arg Leu Glu
225                 230                 235                 240
Glu Ala Leu Met Ala Asp Met Leu Ala His Val Glu Glu Leu Ala Arg
                245                 250                 255
Asp Gly Glu Ala Pro Leu Asp Lys Ala Cys Ala Glu Asp Asp Asp Glu
            260                 265                 270
Glu Asp Glu Glu Glu Glu Glu Glu Glu Pro Asp Pro Asp Pro Glu Met
        275                 280                 285
Glu His Val
    290
```

201 <210> SEQ ID NO: 5
202 <211> LENGTH: 1966
203 <212> TYPE: DNA

RAW SEQUENCE LISTING DATE: 08/08/2001
PATENT APPLICATION: US/09/554,414A TIME: 14:15:37

Input Set : A:\Sequence listing.txt
Output Set: N:\CRF3\08082001\I554414A.raw

```
     204 <213> ORGANISM: Unknown
W--> 206 <220> FEATURE:
W--> 206 <223> OTHER INFORMATION:
     206 <400> SEQUENCE: 5
     207  gggggcgtgg ccccgagaag gcggagacaa gatggccgcc catagcgctt ggaggaccta      60
     208  agaggcggtg gccggggcca cgccccgggc aggagggccg ctctgtgcgc gcccgctcta     120
     209  tgatgcttgc gcgcgtcccc cgcgcgccgc gctgcgggcg gggcgggtct ccgggattcc     180
     210  aagggctcgg ttacggaaga agcgcagcgc cggctgggga gggggctgga tgcgcgcgca     240
     211  cccgggggga ggccgctgct gcccggagca ggaggagggg gagagtgcgg cgggcggcag     300
     212  cggcgctggc ggcgactccg ccatagagca gggggggccag ggcagcgcgc tcgccccgtc     360
     213  cccggtgagc ggcgtgcgca gggaaggcgc tcggggcggc ggccgtggcc gggggcggtg     420
     214  gaagcaggcg ggccggggcg gcggcgtctg tggccgtggc cggggccggg gccgtggccg     480
     215  gggacgggga cggggccggg gccggggccg cggccgtccc ccgagtggcg gcagcggcct     540
     216  tggcggcgac ggcggcggct gcggcggcgg cggcagcggt ggcggcggcg ccccccggcg     600
     217  ggagccggtc cctttcccgt cggggagcgc ggggccgggg cccaggggac cccgggccac     660
     218  ggagagcggg aagaggatgg attgcccggc cctccccccc ggatggaaga aggaggaagt     720
     219  gatccgaaaa tctgggctaa gtgctggcaa gagcgatgtc tactacttca gtccaagtgg     780
     220  taagaagttc agaagcaagc ctcagttggc aaggtacctg ggaaatactg ttgatctcag     840
     221  cagttttgac ttcagaactg gaaagatgat gcctagtaaa ttacagaaga acaaacagag     900
     222  actgcgaaac gatcctctca atcaaaataa gggtaaacca gacttgaata caacattgcc     960
     223  aattagacaa acagcatcaa ttttcaaaca accggtaacc aaagtcacaa atcatcctag    1020
     224  taataaagtg aaatcagacc cacaacgaat gaatgaacag ccacgtcagc ttttctggga    1080
     225  gaagaggcta caaggactta gtgcatcaga tgtaacagaa caaattataa aaaccatgga    1140
     226  actacccaaa ggtcttcaag gagttggtcc aggtagcaat gatgagaccc ttttatctgc    1200
     227  tgttgccagt gctttgcaca caagctctgc gccaatcaca gggcaagtct ccgctgctgt    1260
     228  ggaaaagaac cctgctgttt ggcttaacac atctcaaccc ctctgcaaag cttttattgt    1320
     229  cacagatgaa gacatcagga aacaggaaga gcgagtacag caagtacgca agaaattgga    1380
     230  agaagcactg atggcagaca tcttgtcgcg agctgctgat acagaagaga tggatattga    1440
     231  aatggacagt ggagatgaag cctaagaata tgatcaggta actttcgacc gactttcccc    1500
     232  aagrgaaaat tcctagaaat tgaacaaaaa tgtttccact ggcttttgcc tgtaagaaaa    1560
     233  aaaatgtacc cgagcacata gagcttttta atagcactaa ccaatgcctt tttagatgta    1620
     234  tttttgatgt atatatctat tattcaaaaa atcatgttta ttttgagtcc taggacttaa    1680
     235  aattagtctt ttgtaatatc aagcaggacc ctaagatgaa gctgagcttt tgatgccagg    1740
     236  tgcaatctac tggaaatgta gcacttacgt aaaacatttg tttcccccac agttttaata    1800
     237  agaacagatc aggaattcta aataaatttc ccagttaaag attattgtga cttcactgta    1860
     238  tataaacata tttttatact ttattgaaag gggacacctg tacattcttc catcatcact    1920
     239  gtaaagacaa ataaatgatt atattcacaa aaaaaaaaaa aaaaaa                   1966
     241 <210> SEQ ID NO: 6
     242 <211> LENGTH: 414
     243 <212> TYPE: PRT
     244 <213> ORGANISM: Unknown
W--> 246 <220> FEATURE:
W--> 246 <223> OTHER INFORMATION:
     246 <400> SEQUENCE: 6
     247  Met Arg Ala His Pro Gly Gly Gly Arg Cys Cys Pro Glu Gln Glu Glu
     248   1               5                  10                  15
     249  Gly Glu Ser Ala Ala Gly Gly Ser Gly Ala Gly Gly Asp Ser Ala Ile
     250              20                  25                  30
     251  Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly
```

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/554,414A

DATE: 08/08/2001
TIME: 14:15:38

Input Set : A:\Sequence listing.txt
Output Set: N:\CRF3\08082001\I554414A.raw

L:13 M:201 W: Mandatory field data missing, FILE REFERENCE
L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:30 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:68 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:68 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:127 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:127 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:161 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:161 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:206 M:258 W: Mandatory Feature missing, <220> FEATURE:
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